```
  1  ATTTTATTTATTACCAATCTTATATAATATATTAAATTTCTTACAAAAATCTCTAATG      60
 61  TTTTATACCTAATATATATATTCTGGCTTGTATCTCCACTTCCACTATTGTTAAT       120
121  TTATTTTCACTATTTTAGGTGTAATGAATTGCAAAAATTCTTATAACAACTGCATT      180
                             M  N  C  K  K  I  L  I  T  T  A  L

181  AATATCATTAAATGTACTCTATTCCAAGCCATATCTTTTTCTGATACTATACAAGATGGTAA    240
      I  S  L  M  Y  S  I  P  S  I  S  F  S  D  T  I  Q  D  G  N

241  CATGGGTGGTAACTTCTATATTAGTGGAAAGTATGTACCAAGTGTCTCACATTTGGTAG     300
      M  G  G  N  F  Y  I  S  G  K  Y  V  P  S  V  S  H  F  G  S

301  CTTCTCAGCTAAAGAAGAAAGCAAATCAACTGTTGGAGTTTTTGGATTAAAACATGATTG    360
      F  S  A  K  E  E  S  K  S  T  V  G  V  F  G  L  K  H  D  W

361  GGATGGAAGTCCAATACTTAAGAATAAACACGCTGACTTTACTGTTCCAAACTATTCGTT    420
      D  G  S  P  I  L  K  N  K  H  A  D  F  T  V  P  N  Y  S  F

421  CAGATACGAGAACAATCCATTCTAGGGTTTGCAGGAGCTATCGGTTACTCAATGGGTGG    480
      R  Y  E  N  N  P  F  L  G  F  A  G  A  I  G  Y  S  M  G  G

481  CCCAAGAATAGAATTCGAAATATCTTATGAAGCATTCGACGTAAAAAGTCCTAATATCAA    540
      P  R  I  E  F  E  I  S  Y  E  A  F  D  V  K  S  P  N  I  N

541  TTATCAAAATGACGCGCCACAGGTACTGCGCTCTATCTCATCACACATCGGCAGCCATGGA   600
      Y  Q  N  D  A  H  R  Y  C  A  L  S  H  H  T  S  A  A  M  E

601  AGCTGATAAATTTGTCTTCTTAAAAAACGAAGGGTTAATTGACATATCACTTGCAATAAA    660
      A  D  K  F  V  F  L  K  N  E  G  L  I  D  I  S  L  A  I  N

661  TGCATGTTATGATATAATAAATGACAAAGTACCTGTTTCTCCTTATATATGCGCAGGTAT    720
      A  C  Y  D  I  I  N  D  K  V  P  V  S  P  Y  I  C  A  G  I
```

Fig. 1A

721 TGGTACTGATTTGATTTCTATGTTTGAAGCTACAAGTCCTAAAATTTCCTACCAAGGAAA 780
    G T D L I S M F E A T S P K I S Y Q G K

841 CAGGATCATAGGTAATGAGTTTAGAGATATTCCTGCAATAGTACCTAGTAACTCAACTAC 900
    R I I G N E F R D I P A I V P S N S T T

901 AATAAGTGGACCACAATTGCAACAGTAACACTAAATGTGTCACTTTGGTTTAGAACT 960
    I S G P Q F A T V T L N V C H F G L E L

961 TGGAGGAAGATTAACTTCTAATTTTATTGTTGCCACATATTAAAAATGATCTAAACTTG 1020
    G G R F N F (SEQ. ID NO: 2)

1021 TTTTTAWTATTGCTACATACAAAAAAAGAAAATAGTGGCAAAAGAATGTAGCAATAAGA 1080
1081 GGGGGGGGGACCAAATTTATCTTCTATGCTTCCCAAGTTTTTCYCGCTATTTATGA 1140
1141 CTTAAACAACAGAAGGTAATATCCTCACGGAAAACTTATCTTCAAATATTTTATTTATTA 1200
1201 CCAATCTTATATATAATATAATTAAATTTCTCTTACAAAAATCACTAGTATTTTATACCAAAA 1260
1261 TATATATTCTGACTTGCTTGTCTTTTCTTGCTTTTAATTTTATTTGTCACTAT 1320
1321 TAGGTTATAATAAWATGAATTGCMAAAGATTTTCATAGCAAGTGCATTGATATCCACTAA 1380
1381 TGTCTTTCTTACCTAGCGTATCTTTTTCTGAATCAATACATGAAGATAATATAAATGGTA 1440
1441 ACTTTTACATTAGTGCAAAGTATATGCCAAAGTGCCTCACACTTTGGCGTATTTTCAGTTA 1500
1501 AAGAAGAGAAAAAACAACAACTGGAGTTTTCGGATTAAAACAAGATTGGGACGGAGCAA 1560
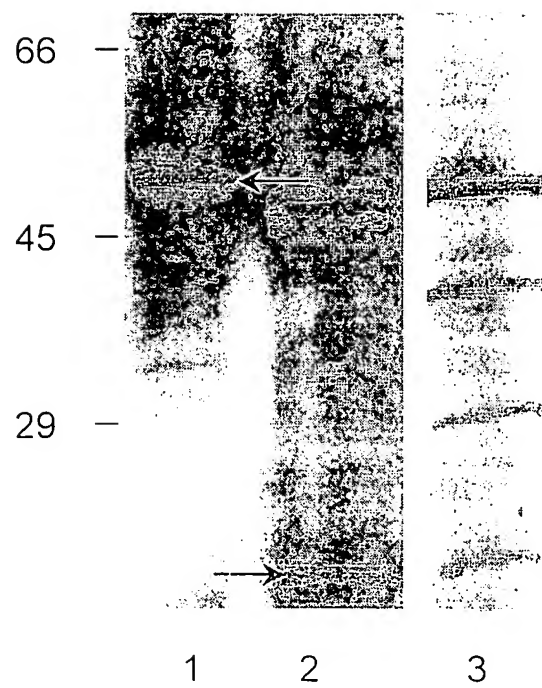1561 CACTAAAGGATGCAAGCWGCAGCWGCCACACAWTAGACCCAAGTACAATG 1607

(SEQ ID NO: 1)

Fig. 1B

66 —

45 —

29 —

1   2   3

Fig. 2

```
                                                    ↓
ECaP28    MNCKKILITTALISLMYSIPSISFSDTIQDGNMG-GN----FYISGKYVPSVSHFGSFSAKE----ESKSTVGVFGLKH   70
ECa28SA2  ...VFTIS....SI.FL.NV.Y.NPVYGNS.-Y...-----......M..P..I...E.....----.K.K.TV.Y...E   70
ECa28SA1  .KY.TFTV..VL.TSFTHF.P.YSPARASTIH--..-----......M.TA..I....-----....QSF.KVLV..DQ   69
EChP28    ..Y..VF..S....IS.L.GV....PA-GSGIN-...-----....M..A...V......----.-----RNT......Q   69
OMP-1B    ..Y...FVSS....SIL.YQ..A.PVTSNDT.INDSREG....V..N..I...RK...E.APINGNTSI.KK.....K   80
OMP-1C    ....FF.....ALP.SFL.G.LL.EPV..DSVS-.....-----....M..A...V...-----....KNP..ALY...Q   70
OMP-1D    ..E.FF.....TL..SFL.G..L..PV..D.IS-.....-----....M..A...V...-----....RNT....IEQ   70
OMP-1E    ...FF.....V...SFL.G......PV.GD.IS-..V...-----....M..A...M...-----....KNP..ALY...Q   70
OMP-1F    ...FF....T.V...SFL.G......AV.ND.V.-.....-----....V...Q.....-----....RNT.T.....Q   70
MAP-1     ..F..ST....VSFL.GV......V..EE.NPV.S-----V..A..M.TA....KM.I.....-----.D.RD.KA.....K   71
                                                              VR1

ECaP28    DWDGSPILKNKHAD-FTVPNYSFRYENNPFLGFAGAIGYSMGGPRIEFEISYEAFDVKSPNINYQNDAH--RYCALSH--   145
ECa28SA2  N.A.DA.SSQSPD.N..IR....K.AS.K.....V.....I.S..V.M......NQGN.   (SEQ ID NO: 7)        133
ECa28SA1  RLSHNI.NN.DT.KSLK.Q...K.K........I.NS..L.V.H.I..T.N.GN..L..S..-K.....GS             147
EChP28    N....A.SNSSPN.V...S....K..........D...L.V..T....NQGN..K.E...-                       145
OMP-1B    .----GDIAQSAN.NRTDPALEFQ..LIS..S.S...A.D...L.AA.QK..A.N.DN.DT.SGDYYK.FG..RED        154
OMP-1C    ..N.-VSASSHADAD.NNKG....K.........V...T.....NQGG..K....-----.DR--                   145
OMP-1D    ..RCV.SRTTLS.I.......K....K......V.....L.V....NQGN..K.E....-.Y---                    146
OMP-1E    ..E.-ISSSHNDNH.NNKG...K..........V......V....NQGN..K.....-----.GQ--                 145
OMP-1F    ....T.S..SPENT.N.....K..........V.L.N...LM..T....NQGN..K...----K.Y..T.-             146
MAP-1     ....VKTPSGNTNSI..EKD...K..........V.......N......T.....RN.GG..K....-----M....        145
                VR2
```

Fig. 3A

```
ECaP28    ---HTSAAME-----ADKFVFLKNEGLIDISLAINACYDIINDKVPVSPYICAGIGTDLISMFEATSPKISYQGKLGISY   217
ECa28SA2                                                                                     133
ECa28SA1  HICSDGNSGDWYTAKT...L.........L.V.FML..........TTE.M.F.........LN.                    227
EChP28    -----NS.ADMSSASNN.........L...FML........V.........L.                                219
OMP-1B    AI-------------ADK.Y.V...ITFM.MV.T.TAEG..FI..A...NV.KDFNL.F......I.                  222
OMP-1C    ----KA.ST--NAT.SHY.L.....L...ML........V.........IN.                                 218
OMP-1D    ---LLGTETQIDGAGSAS...I...L.K.FML...V.SEGI.F.........IN.                              222
OMP-1E    ---QDNSG---IPKTS.Y.L.S...L...FML......I.V.........N.                                 218
OMP-1F    -----NSGGKLSNAG.........L...ML........V.........IN.                                  220
MAP-1     -----DT.SSSTAG.TTS.MV..N.T....ML.......V.VIN..N..L.                                  219
                          VR3

ECaP28    SINPETSVFIGGHFHRIIGNEFRDIPA---IVPSNSTTISGPQF-ATVTLNVCHFGLELGGRFNF   (SEQ ID NO:2)   278
ECa28SA2                                                                                      133
ECa28SA1  T..SRV...A.....KG..T---LL.DG.NIKVQQS--.....D.........I.S..F.        (SEQ ID NO:8)   287
EChP28    ..S..A.....KV.....T---.I.TG..LAGKGNYP.I.I.D.......I.....A.           (SEQ ID NO:9)   281
OMP-1B    P.T..V.A...YY.GV...N.NK..VITPV.LEGAPQTTS---.L..IDTGY.G.V.V..T.       (SEQ ID NO:10)  283
OMP-1C    .....A...V.....KVA..........ST---LKAFATPSSAATPDL.......S...V.        (SEQ ID NO:11)  280
OMP-1D    P.S..A.....KV..........T---MI..E.ALAGKGNYP.I...D.FY.I..........QL.   (SEQ ID NO:12)  286
OMP-1E    .....A.....KV..........T---LKAFVTSS--ATPDL.I......S.                 (SEQ ID NO:13)  278
OMP-1F    ..S..A...V.....KV..........-MI..T.LTGN-H.-TI...S......V.             (SEQ ID NO:14)  280
MAP-1     .....A.I.......V.......K.ATSKVFTS.GNASSAVSPGF.SAI.D......I.I......V.  (SEQ ID NO:15)  284
                                  VR4
```

Fig. 3B

Fig. 4

Fig. 5

Surface
Probability

Surface Regions

Antigenic Index

T-cell Motif

Amino Acid

E. canis P28 (Jake)

Surface
Probability

Surface Regions

Antigenic Index

T-cell Motif
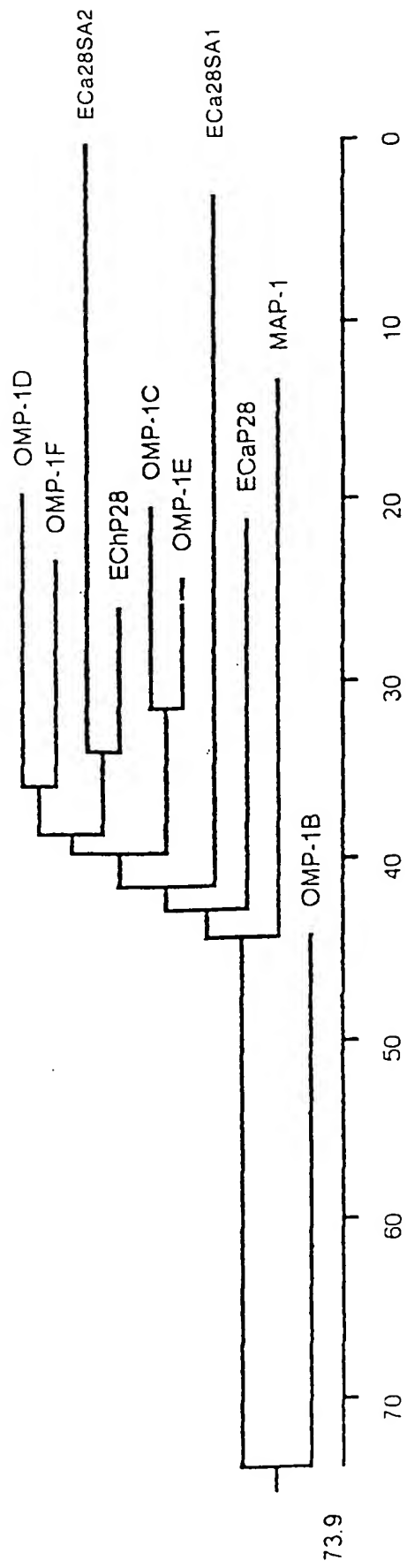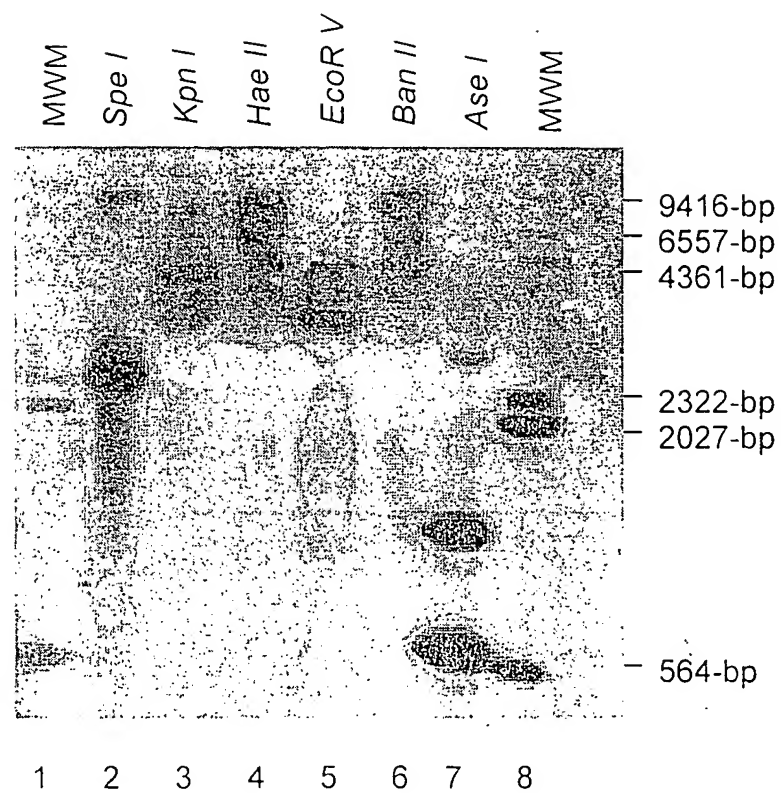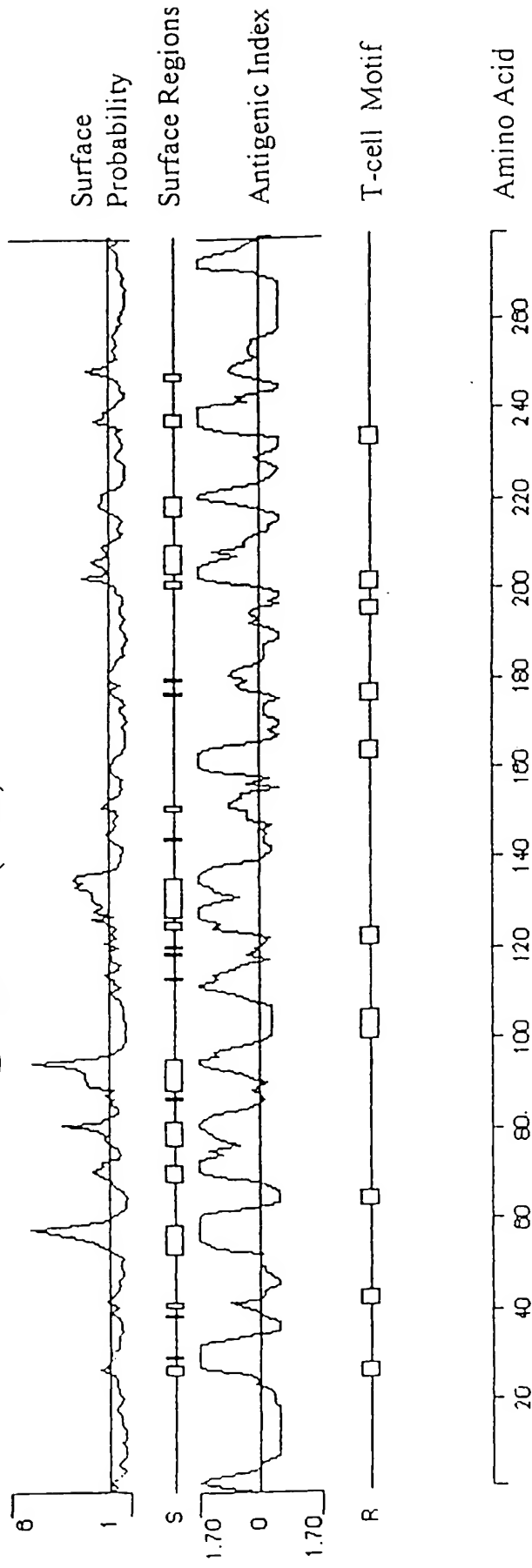
E. chaffeensis P28 (Arkansas)

20 40 60 80 100 120 140 160 180 200 220 240 260

Fig. 6

Eca28SA2

ATGAATTGTAAAAAAGTTTTCACAATAAGTGCATTGATATCATCCATATACTTCCTACCT 60
 M N C K K V F T I S A L I S S I Y F L P

AATGTCTCATACTCTAACCCAGTATATGGTAACAGTATGTATGGTAATTTTTACATATCA 120
 N V S Y S N P V Y G N S M Y G N F Y I S

GGAAAGTACATGCCAAGTGTTCCTCATTTTGGAATTTTTTCAGCTGAAGAAGAGAAAAAA 180
 G K Y M P S V P H F G I F S A E E E K K

AAGACAACTGTAGTATATGGCTTAAAAGAAAACTGGGCAGGAGATGCAATATCTAGTCAA 240
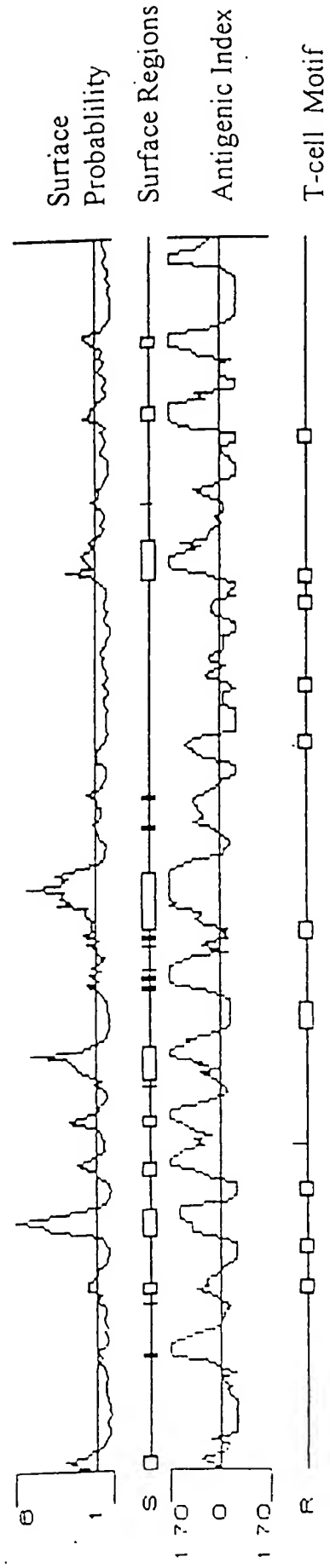 K T T V V Y G L K E N W A G D A I S S Q

AGTCCAGATGATAATTTTACCATTCGAAATTACTCATTCAAGTATGCAAGCAACAAGTTT 300
 S P D D N F T I R N Y S F K Y A S N K F

TTAGGGTTTGCAGTAGCTATTGGTTACTCGATAGGCAGTCCAAGAATAGAAGTTGAGATG 360
 L G F A V A I G Y S I G S P R I E V E M

TCTTATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGG 420
 S Y E A F D V K N P G D N Y K N G A Y R

TATTGTGCTTTATCTCATCAAGATGATGCGGATGATGACTAGTGCAACTGACAAA 480
 Y C A L S H Q D D A D D D M T S A T D K

TTTGTATATTAATTAATGAAGGATTACTTAACATATCATTTATGACAAACATATGTTAT 540
 F V Y L I N E G L L N I S F M T N I C Y

GAAAACAGCAAGCAAAAATATACCTCTCTCCTTACATATGTGCCAGGTATTGGTACTGAT 600
 E T A S K N I P L S P Y I C A G I G T D

TTAATTCACATGTTTGAAACTACACATCCTAAAATTTCTTATCAAGGAAAGCTAGGGTTG 660
 L I H M F E T T H P K I S Y Q G K L G L

Fig. 7A

GCCTACTTCGTAAGTGCAGAGTCTTCGGTTGTTCTTTGGTATATATTTCATAAAATTATA 720
A Y F V S A E S S V S F G I Y F H K I I

AATAATAAGTTTAAAAAATGTTCCAGCCATGGTACCCTATTAACTTCAGACGACGAGATAGTAGGA 780
N N K F K N V P A M V P I N S D E I V G

CCACAGTTTGCAACAGTAACATTAAATGTATGCTACTTTGGATTAGAACTTGGATGTAGG 840
P Q F A T V T L N V C Y F G L E L G C R

TTCAACTTCTAATTTCGTGGTACACATATCACGAAGCTAAAATTGTTTTTTATCTCTGC 900
F N F * (SEQ ID NO: 4)

(SEQ ID NO: 3)

TGTATACAAGAGAAAAATAGTAGTGAAAATTACCTAACAATATGACAGTACAAGTTTAC 960
CAAGCTTATTCTCACAAAACTTCTTGTGTCTTTATCTCTTTACAATGAAATGTACACTT 1020
AGCTTCACTACTGTAGAGTGTGTTATCAATGCTTGTTTATTATTATACTCTACATAATAT 1080
GTTAAATTTTTCTTACAAAACTCACTACTAGTAATTATACTAGAATATATATTCTGACTTGT 1140

(SEQ ID NO: 31)

ECa28SA3

ATTTGCTTTATACTTCCACTATTGTTAATTTATTTTCACTATTTTAGGTGTAATATGAAT 1200
                                                    M N

TGCAAAAAAATTCTTATAACAACTGCATTAATGTCATTAATGTACTATGCTCCAAGCATA 1260
C K K I L I T T A L M S L M Y Y A P S I

TCTTTTTCTGATACTATACAAGAGACGATAACACTGGTAGCTTCTACATCAGTGGAAAATAT 1320
S F S D T I Q D D N T G S F Y I S G K Y

GTACCAAGTGTTCACATTTGGTGTTTCTCAGCTAAAGAAGAAACTCAACTGTT 1380
V P S V S H F G V F S A K E E R N S T V

GGAGTTTTGGATTAAAACATGATGGAATGGAAGTGGAGGTACAATATCTAACTCTTCTCCAGAA 1440
G V F G L K H D W N G G T I S N S S P E

Fig. 7B

AATATATTCACAGTTCAAAAATTATTCGTTTAAATACGAAAAACAACCCATTCTTAGGGTTT 1500
N I F T V Q N Y S F K Y E N N P F L G F

GCAGGAGCTATTGGTTATTCAATGGGTGGCCCAAGAATAGAACTTGAAGTTCTGTACGAG 1560
A G A I G Y S M G G P R I E L E V L Y E

ACATTCGATGTGTGAAAAATCAGAACAATAATTATAAGAACGGGCGCCACACAGATACTGTGCT 1620
T F D V K N Q N N Y K N G A H R Y C A

TTATCTCATCATAGTTCAGCAACAAGCATGTCCTCCGCAAGTAACAAATTTGTTTTCTTA 1680
L S H H S S A T S M S S A S N K F V F L

AAAAATGAAGGGTTAATTGACTTATCATTTATGATAAATGCATGCTATGACATAATAATT 1740
K N E G L I D L S F M I N A C Y D I I I

GAAGGAATGCCTTTTTCACCTTATATTGTGCAGGTGTTGGTACTGATGTGTTGTTTCCATG 1800
E G M P F S P Y I C A G V G T D V V S M

TTTGAAGCTATAAATCCTAAAATTTCTTACCAAGGAAAACTAGGATTAGGTTATAGTATA 1860
F E A I N P K I S Y Q G K L G L G Y S I

AGTTCAGAAGCCTCTGTTTTTATCGGTGGACACTTTCACAGAGTCATAGGTAATGAATTT 1920
S S E A S V F I G G H F H R V I G N E F

AGAGACATCCCTGCTATGGTTCCTAGTGGATCAAATCTTCCAGAAAACCAATTTGCAATA 1980
R D I P A M V P S G S N L P E N Q F A I
(SEQ ID NO: 5)

GTAACACTAAAATGTGTGTCACTTTGGCATAGAACTTGGAGGAAGATTTAACTTCTGA 2031
V T L N V C H F G I E L G G R F N F *
(SEQ ID NO: 6)

Fig. 7C

ECa28SA1 NC1 ECa28SA2 NC2 ECa28SA3 NC3 ECa28-1 NC4 ECa28-2

Characterized Region

861 bp   299 bp   849 bp   345 bp   840 bp   345 bp   834 bp   355 bp   864 bp
287 aa   283 aa   280 aa   278 aa   288 aa

Locus-1   Locus-2

Fig. 8

ECa28-1

ECa28SA3

ECa28-2

ECa28SA1

ECa28SA2

52.3   50   40   30   20   10   0
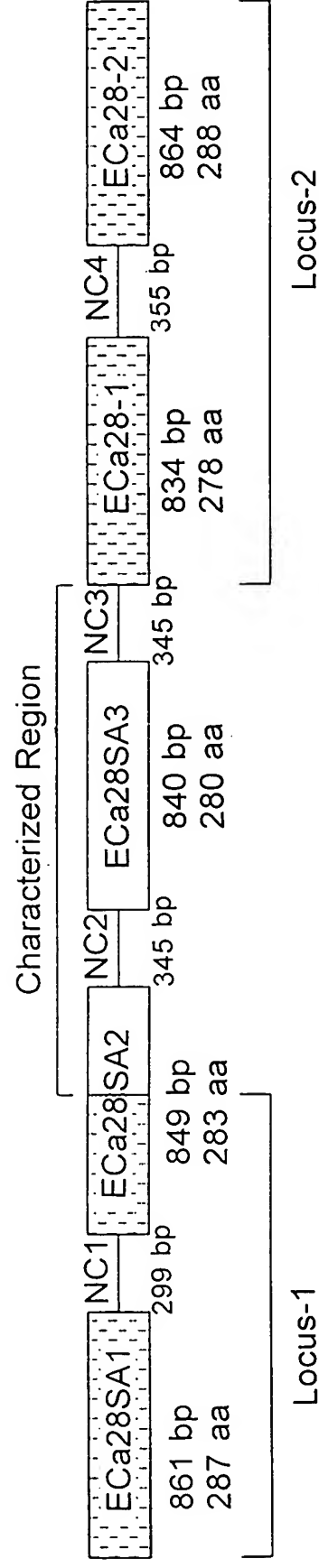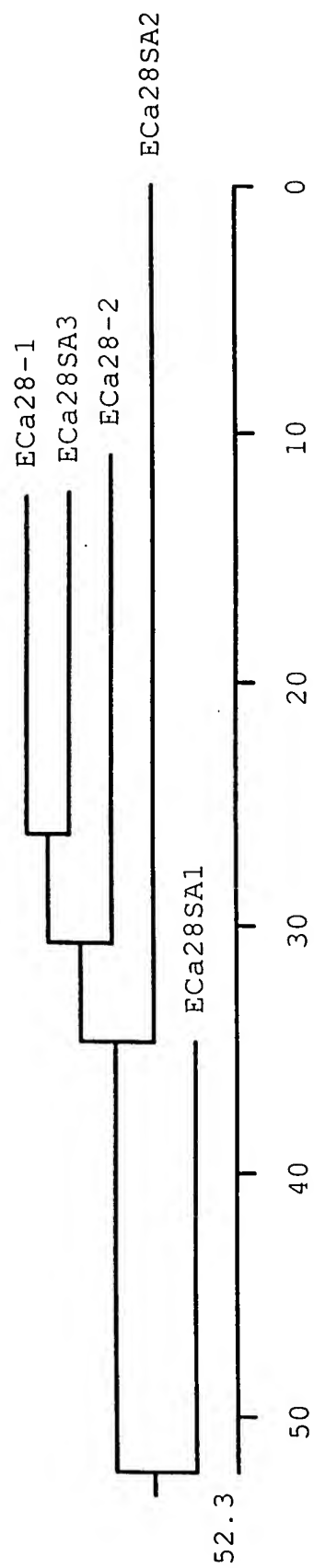
Fig. 9

```
  1  TAATACTTCTATTGT-ACATGTTAAAAATAGTACTAGTTTGCTTCTGTGGTT--TATAAACGCAAGAGAGAA--         28nc1
  1  ....TTCGTGG.A--C....A.C.CG...-GC..AA.T.G.TT..T.A.CTC.GC.G..T..AAG..A.A...TA         28nc2
  1  .G..TT.AT.G...CC.....A.........GA.CTA.AC...T..T.A.TA..GC..C.T..AA..A.A....AA         28nc3
  1  ....TT.AT.G...CC.....A.........GA.CTA.AC...T..T.AWTA..GC..C.T..AA..A.A--...AA         28nc4

 70  ATAGT-------TAGTAATAAATTAGAAAG------TTAAA--TATT---AGAAAAGT-CA                       28nc1
 72  G...G--AAAATTACC..AC....TGAC..T.CAAGTTTACC..GCT...CTC.C...C.T.T                     28nc2
 75  .....GGCAAAAGAATG...C.....GAGG.GGG.GGGGGAC...TT...CCTTC--T.TTC.T.T                  28nc3
 74  .....GGCAAAAGAATG...C.....GAGG.GGG.GGGGGACC...TT...CTTC--T.TGC.T.C                  28nc4

112  TATGTTTTTCATTGTCATTGAT-ACTCAACTA----AAAGTAGTAT------------AAATGT------------       28nc1
136  .G..C...T..CTCT--.T.CA.-.G..A.-GTAC.-CT..CT.CACTACTGTAG.G...GTTTATCAATGC           28nc2
139  A..A..C..T--ACT..------T....A.GCAC..CTC.A.GCTTCCA-GG-A....A.GT-TTCTAATAT           28nc3
138  C.A......TCYC.CT...T.G...T.AC.ACAG..G..A...CCTCACGG-A....CT.ATCTTCAAATAT           28nc4

159  --TACTTATTAATAAT-TTTACGTAGTATATTAAAATTCCCTTACAAAAGCCACTAGTATTTTATA                 28nc1
205  TT.GT.......--C.C..A.A..G........TT.......CT..A........                            28nc2
202  TT..T......CC...CC...TA..A...........T........AT.T..A.G.........                    28nc3
211  TT..T......CC...C--...TA..A...........T..........AT..........                       28nc4

222  CTAAAAAGC-TATACTTTGGCTTGTATTTAATTTGTATTTTTACTACTGTTAATTTACTT-TCACTGTT---TCT         28nc1
269  -T.G.ATA...T.C.A.........GC..A.C.CC....T........T..-......A.---..TA                 28nc2
268  ..T..TATA..T.C...........C....C.C.CC....T.......T..-......A.---..TA                 28nc3
276  .C--...ATA...T.C.A.....CT..CT_C_C_C.C...T.T..........T.G.....A..AGG..TA             28nc4
                                      -35                                -10

292  GGTGTAAAT  28nc1   (SEQ ID NO: 30)
338  ........-  28nc2   (SEQ ID NO: 31)
339  .......-.  28nc3   (SEQ ID NO: 32)
339  TA-A...-W  28nc4   (SEQ ID NO: 33)
     RBS
```

Fig. 10

p28-1 879-bp
p28-2 840-bp
p28-3 828-bp
p28-4 861-bp
p28-5 849-bp
p28-6 840-bp
p28-7 834-bp
p28-8 864-bp
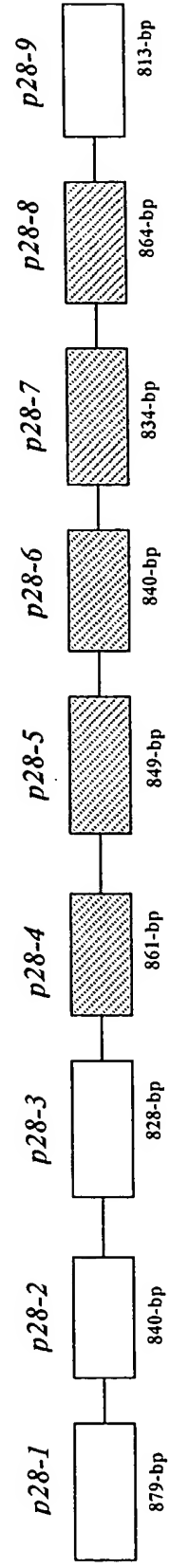p28-9 813-bp

Fig. 11

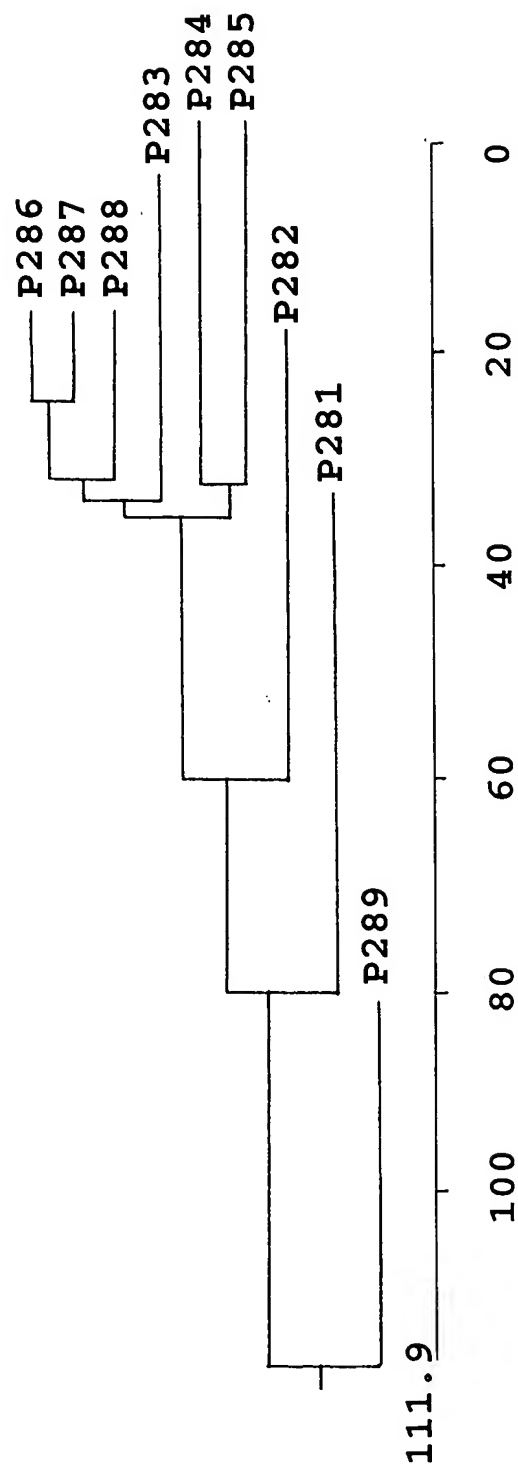Fig. 12

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ATGAATAATAAACTCAAATTTACTATAATAAACACAGTATTAGTATGCTTATTGTCATTA 60
M   N   N   K   L   K   F   T   I   I   N   T   V   L   V   C   L   L   S   L

CCTAATATATCTTCCTCAAAGGCCATAAACAATAACGCTAAAAAGTACTACGGATTATAT 120
P   N   I   S   S   S   K   A   I   N   N   N   A   K   K   Y   Y   G   L   Y

ATCAGTGGACAATATAAACCCAGTGTTTCTGTTTTCAGTAATTTTTCAGTTAAAGAAACC 180
I   S   G   Q   Y   K   P   S   V   S   V   F   S   N   F   S   V   K   E   T

AATGTCATAACTAAAAACCTTATAGCTTTAAAAAAAGATGTTGACTCTATTGAAACCAAG 240
N   V   I   T   K   N   L   I   A   L   K   K   D   V   D   S   I   E   T   K

ACTGATGCCAGTGTAGGTATTAGTAACCCATCAAATTTTACTATCCCCTATACAGCTGTA 300
T   D   A   S   V   G   I   S   N   P   S   N   F   T   I   P   Y   T   A   V

TTTCAAGATAATTCTGTCAATTTCAATGGAACTATTGGTTACACCTTTGCTGAAGGTACA 360
F   Q   D   N   S   V   N   F   N   G   T   I   G   Y   T   F   A   E   G   T

AGAGTTGAAATAGAAGGTTCTTATGAGGAATTTGATGTTAAAAACCCTGGAGGCTATACA 420
R   V   E   I   E   G   S   Y   E   E   F   D   V   K   N   P   G   G   Y   T

CTAAGTGATGCCTATCGCTATTTTGCATTAGCACGTGAAATGAAAGGTAATAGTTTTACA 480
L   S   D   A   Y   R   Y   F   A   L   A   R   E   M   K   G   N   S   F   T

CCTAAAGAAAAAGTTTCTAATAGTATTTTTCACACTGTAATGAGAAATGATGGATTATCT 540
P   K   E   K   V   S   N   S   I   F   H   T   V   M   R   N   D   G   L   S

ATAATATCTGTTATAGTAAATGTTTGCTACGATTTCTCTTTGAACAATTTGTCAATATCG 600
I   I   S   V   I   V   N   V   C   Y   D   F   S   L   N   N   L   S   I   S

CCTTACATATGTGGAGGAGCAGGGGGTAGATGCTATAGAATTCTTCGATGTATTACACATT 660
P   Y   I   C   G   G   A   G   V   D   A   I   E   F   F   D   V   L   H   I

AAGTTTGCATATCAAAGCAAGCTAGGTATTGCTTATTCTCTACCATCTAACATTAGTCTC 720
K   F   A   Y   Q   S   K   L   G   I   A   Y   S   L   P   S   N   I   S   L

TTTGCTAGTTTATATTACCATAAAGTAATGGGCAATCAATTTAAAAATTTAAATGTCCAA 780
F   A   S   L   Y   Y   H   K   V   M   G   N   Q   F   K   N   L   N   V   Q

CATGTTGCTGAACTTGCAAGTATACCTAAAATTACATCCGCAGTTGCTACACTTAATATT 840
H   V   A   E   L   A   S   I   P   K   I   T   S   A   V   A   T   L   N   I

GGTTATTTTGGAGGTGAAATTGGTGCAAGATTGACATTT    (SEQ ID No. 39)    879
G   Y   F   G   G   E   I   G   A   R   L   T   F    (SEQ ID NO. 40)
```

Fig. 13

```
ATGAATTATAAGAAAATTCTAGTAAGAAGCGCGTTAATCTCATTAATGTCAATCTTACCA  60
 M  N  Y  K  K  I  L  V  R  S  A  L  I  S  L  M  S  I  L  P

TATCAGTCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC  120
 Y  Q  S  F  A  D  P  V  G  S  R  T  N  D  N  K  E  G  F  Y

ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAAACT  180
 I  S  A  K  Y  N  P  S  I  S  H  F  R  K  F  S  A  E  E  T

CCTATTAATGGAACAAATTCTCTCACTAAAAAAGTTTTCGGACTAAAGAAAGATGGTGAT  240
 P  I  N  G  T  N  S  L  T  K  K  V  F  G  L  K  K  D  G  D

ATAACAAAAAAAGACGATTTTACAAGAGTAGCTCCAGGCATTGATTTTCAAAATAACTTA  300
 I  T  K  K  D  D  F  T  R  V  A  P  G  I  D  F  Q  N  N  L

ATATCAGGATTTTCAGGAAGTATTGGTTACTCTATGGACGGACCAAGAATAGAACTTGAA  360
 I  S  G  F  S  G  S  I  G  Y  S  M  D  G  P  R  I  E  L  E

GCTGCATATCAACAATTTAATCCAAAAAACACCGATAACAATGATACTGATAATGGTGAA  420
 A  A  Y  Q  Q  F  N  P  K  N  T  D  N  N  D  T  D  N  G  E

TACTATAAACATTTTGCATTATCTCGTAAAGATGCAATGGAAGATCAGCAATATGTAGTA  480
 Y  Y  K  H  F  A  L  S  R  K  D  A  M  E  D  Q  Q  Y  V  V

CTTAAAAATGACGGCATAACTTTTATGTCATTGATGGTTAATACTTGCTATGACATTACA  540
 L  K  N  D  G  I  T  F  M  S  L  M  V  N  T  C  Y  D  I  T

GCTGAAGGAGTATCTTTCGTACCATATGCATGTGCAGGTATAGGAGCAGATCTTATCACT  600
 A  E  G  V  S  F  V  P  Y  A  C  A  G  I  G  A  D  L  I  T

ATTTTTAAAGACCTCAATCTAAAATTTGCTTACCAAGGAAAAATAGGTATTAGTTACCCT  660
 I  F  K  D  L  N  L  K  F  A  Y  Q  G  K  I  G  I  S  Y  P

ATCACACCAGAAGTCTCTGCATTTATTGGTGGATACTACCATGGCGTTATTGGTAATAAA  720
 I  T  P  E  V  S  A  F  I  G  G  Y  Y  H  G  V  I  G  N  K

TTTGAGAAGATACCTGTAATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACATCT  780
 F  E  K  I  P  V  I  T  P  V  V  L  N  D  A  P  Q  T  T  S

GCTTCAGTAACTCTTGACGTTGGATACTTTGGCGGAGAAATTGGAATGAGGTTCACCTTC  840
                                              (SEQ ID No. 41)
 A  S  V  T  L  D  V  G  Y  F  G  G  E  I  G  M  R  F  T  F
                                              (SEQ ID No. 42)
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Fig. 14

ATGAACTGTAAAAAAATTCTTATAACAACTACATTGGTATCACTAACAATTCTTTTACCT 60

M   N   C   K   K   I   L   I   T   T   T   L   V   S   L   T   I   L   L   P

GGCATATCTTTCTCCAAACCAATACATGAAAACAATACTACAGGAAACTTTTACATTATT 120

G   I   S   F   S   K   P   I   H   E   N   N   T   T   G   N   F   Y   I   I

GGAAAATATGTACCAAGTATTTCACATTTTGGGAACTTTTCAGCTAAAGAAGAAAAAAAC 180

G   K   Y   V   P   S   I   S   H   F   G   N   F   S   A   K   E   E   K   N

ACAACAACTGGAATTTTTGGATTAAAAGAATCATGGACTGGTGGTATCATCCTTGATAAA 240

T   T   T   G   I   F   G   L   K   E   S   W   T   G   G   I   I   L   D   K

GAACATGCAGCTTTTAATATCCCAAATTATTCATTTAAATATGAAAATAATCCATTTTTA 300

E   H   A   A   F   N   I   P   N   Y   S   F   K   Y   E   N   N   P   F   L

GGATTTGCAGGGGTAATTGGCTATTCAATAGGTAGTCCAAGAATAGAATTTGAAGTATCA 360

G   F   A   G   V   I   G   Y   S   I   G   S   P   R   I   E   F   E   V   S

TACGAGACATTCGATGTACAAAATCCAGGAGATAAGTTTAACAATGATGCACATAAGTAT 420

Y   E   T   F   D   V   Q   N   P   G   D   K   F   N   N   D   A   H   K   Y

TGTGCTTTATCCAATGATTCCAGTAAAACAATGAAAAGTGGTAAATTCGTTTTTCTCAAA 480

C   A   L   S   N   D   S   S   K   T   M   K   S   G   K   F   V   F   L   K

AATGAAGGATTAAGTGACATATCACTCATGTTAAATGTATGTTATGATATAATAAACAAA 540

N   E   G   L   S   D   I   S   L   M   L   N   V   C   Y   D   I   I   N   K

AGAATGCCTTTTTCACCTTACATATGTGCAGGCATTGGTACTGACTTAATATTCATGTTT 600

R   M   P   F   S   P   Y   I   C   A   G   I   G   T   D   L   I   F   M   F

GACGCTATAAACCATAAAGCTGCTTATCAAGGAAAATTAGGTTTTAATTATCCAATAAGC 660

D   A   I   N   H   K   A   A   Y   Q   G   K   L   G   F   N   Y   P   I   S

CCAGAAGCTAACATTTCTATGGGTGTGCACTTTCACAAAGTAACAAACAACGAGTTTAGA 720

P   E   A   N   I   S   M   G   V   H   F   H   K   V   T   N   N   E   F   R

GTTCCTGTTCTATTAACTGCTGGAGGACTCGCTCCAGATAATCTATTTGCAATAGTAAAG 780

V   P   V   L   L   T   A   G   G   L   A   P   D   N   L   F   A   I   V   K

TTGAGTATATGTCATTTTGGGTTAGAATTTGGGTACAGGGTCAGTTTT(SEQ ID No. 43)828

L   S   I   C   H   F   G   L   E   F   G   Y   R   V   S   F   (SEQ ID NO. 44)

Fig. 15

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ATGAATTACAAAAGATTTGTTGTAGGTGTTACGCTGAGTACATTTGTTTTTTTCTTATCT  60
 M   N   Y   K   R   F   V   V   G   V   T   L   S   T   F   V   F   F   L   S

GATGGTGCTTTTTCTGATGCAAATTTTTCTGAAGGGAGGAGAGGACTTTATATAGGTAGT  120
 D   G   A   F   S   D   A   N   F   S   E   G   R   R   G   L   Y   I   G   S

CAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGT  180
 Q   Y   K   V   G   I   P   N   F   S   N   F   S   A   E   E   T   I   P   G

ATTACAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAAT  240
 I   T   K   K   I   F   A   L   G   L   D   K   S   E   I   N   T   H   S   N

TTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATT  300
 F   T   R   S   Y   D   P   T   Y   A   S   S   F   A   G   F   S   G   I   I

GGATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGAACCT  360
 G   Y   Y   V   N   D   F   R   V   E   F   E   G   S   Y   E   N   F   E   P

GAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCGAAAT  420
 E   R   Q   W   Y   P   E   N   S   Q   S   Y   K   F   F   A   L   S   R   N

GCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCT  480
 A   T   N   S   D   N   K   F   I   V   L   E   N   N   G   V   V   D   K   S

CTTAATGTAAATGTTTGTTATGATATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATG  540
 L   N   V   N   V   C   Y   D   I   A   S   G   S   I   P   L   A   P   Y   M

TGTGCTGGTGTTGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCT  600
 C   A   G   V   G   A   D   Y   I   K   F   L   G   I   S   L   P   K   F   S

TATCAAGTTAAGTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGG  660
 Y   Q   V   K   F   G   V   N   Y   P   L   N   V   N   T   M   L   F   G   G

GGTTATTACCATAAGGTTGTAGGTGATAGGCATGAGAGAGTAGAAATAGCTTACCATCCT  720
 G   Y   Y   H   K   V   V   G   D   R   H   E   R   V   E   I   A   Y   H   P

ACTGCATTATCTGACGTTCCTAGAACTACTTCAGCTTCTGCTACTTTAAATACTGATTAT  780
 T   A   L   S   D   V   P   R   T   T   S   A   S   A   T   L   N   T   D   Y

TTTGGTTGGGAGATTGGATTTAGATTTGCGCTA  (SEQ ID No. 45)            813
 F   G   W   E   I   G   F   R   F   A   L     (SEQ ID No. 46)
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Fig. 16